## Claims

1. A method of labeling individual mammalian chromosomes in mitotic cells or in interphase cells by in situ hybridization with chromosome-specific probes, to produce a chromosome-specific signal.

2. A method of labeling individual human chromosomes in mitotic cells or in interphase cells by in situ hybridization with chromosome-specific probes, to produce a chromosome-specific signal.

3. A method of producing highly specific decoration of an individual human target chromosome, comprising in situ suppression hybridization of labeled DNA probes, which are chromosome specific, to DNA in human mitotic cells or in human interphase cell.

4. A method of Claim 3, wherein the DNA probes are selected from the group consisting of total recombinant library DNA, DNA inserts purified from a chromosome-derived recombinant DNA library, and specific DNA fragments derived from chromosomes.

5. A method of Claim 4, wherein the labeled DNA probes are selected from the group consisting of: DNA probes labeled with at least one

fluorochrome; DNA probes labeled with at least one member of a specific binding pair; and DNA probes labeled with an enzyme.

6. A method of Claim 5, wherein the fluorochrome is selected from the group consisting of fluorescein, rhodamine, Texas red, Lucifer yellow, phycobiliproteins and cyanin dyes and the member of a specific binding pair is biotin.

7. A method of assessing chromosome abberations in human cells by chromosomal in situ supression hybridization.

8. A method of Claim 7, wherein the human cells are selected from the group consisting of metaphase cells, prophase cells and interphase cells.

9. A method of detecting chromosome aberrations in human aneuploid cells, comprising
a) combining
1) the human aneuploid cells, treated so as to render nucleic acid sequences present available for hybridization with complementary nucleic acid sequences; and
2) a hybridization mixture comprising labeled human DNA derived from a specific chromosome; competitor DNA; and nonhuman genomic DNA, under conditions appropriate

for hybridization of complementary nucleic acid sequences to occur; and

b) detecting labeled human DNA derived from the specific chromosome hybridized to nucleic acid sequences from the aneuploid cells.

10. A method of Claim 9, wherein the aneuploid cells are human tumor cells.

11. A method of Claim 10, in which the human tumor cells are selected from the group consisting of: metaphase cells, prophase cells and interphase cells.

12. A method of Claim 10, wherein the human tumor cell is a human glioma cell.

13. A method of detecting in a sample numerical alterations in a human chromosome present in the sample, comprising:

a) combining

1) the sample, treated so as to render nucleic acid sequences present in the sample available for hybridization with complementary nucleic acid sequences; and

2) a hybridization mixture comprising labeled human DNA derived from the selected chromosome; competitor DNA; and nonhuman genomic DNA, under conditions appropriate for hybridization of

complementary nucleic acid sequences to occur; and

b) detecting labeled DNA derived from the selected chromosome hybridized to nucleic acid sequences present in the sample.

14. A method of Claim 13, wherein the selected human chromosome is selected from the group consisting of the following chromosomes: 13, 18, 21, X and Y.

15. A method of Claim 13, wherein the selected human chromosome is chromosome number 21 and the labeled human DNA derived from the selected chromosome is DNA inserts purified from a chromosome-derived recombinant DNA library.

16. A method of determining over-representation or under-representation of a selected chromosome or a portion thereof in human tumor cells, comprising the steps of:

a) combining

1) human tumor cells, treated so as to render nucleic acid sequences present in the cells available for hybridization with complementary nucleic acid sequences; and

2) a hybridization mixture comprising labeled DNA fragments derived from a selected chromosome; competitor DNA; and nonhuman genomic DNA, under conditions appropriate for hybridization of

complementary nucleic acid sequences to occur; and

b) detecting labeled human chromosome-specific DNA fragments hybridized to nucleic acid sequences from the tumor cells.

17. A method of identifying chromosome-specific DNA present in a selected mammalian chromosome, comprising:

a) combining the following substances:

1) the selected mammalian chromosome;

2) DNA fragments derived from the selected mammalian chromosome bearing a detectable label;

3) competitor DNA; and

4) carrier DNA,

under conditions appropriate for hybridization of complementary nucleic acid sequences to occur; to form a complex of the DNA fragments bearing a detectable label with the selected mammalian chromosome; and

b) detecting complexes formed in step (a).

18. A method of Claim ~~17~~, further comprising isolation of chromosome-specific DNA in a selected mammalian chromosome by separating the selected complexes formed from the remaining substances combined in step (a).

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